

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE GENERAL HOSPITAL CORPORATION  
FRUIT STREET  
BOSTON, MA 02114  
UNITED STATES OF AMERICA

APPLICANT/INVENTOR: de la Monte, Suzanne  
Wands, Jack R.

(ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
(B) STREET: 1100 New York Ave., Suite 600  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,908  
(B) FILING DATE: 26-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.  
(B) REGISTRATION NUMBER: 32,893  
(C) REFERENCE/DOCKET NUMBER: 0609.437PC01

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600  
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

00964638 092801  
F00260" 82949660



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|   |     |
|---|-----|
| TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC | 50  |
| Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys                 |     |
| 1 5 10  |     |
| AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC | 98  |
| Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser |     |
| 15 20 25  |     |
| GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC | 146 |
| Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys |     |
| 30 35 40  |     |
| ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT | 194 |
| Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe |     |
| 45 50 55 60   |     |
| CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC | 242 |
| Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro |     |
| 65 70 75  |     |
| TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC | 290 |
| Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala |     |
| 80 85 90  |     |
| CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG | 338 |
| Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met |     |
| 95 100 105  |     |
| TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC | 386 |
| Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu |     |
| 110 115 120   |     |
| CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT | 434 |
| Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile |     |
| 125 130 135 140   |     |
| TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG | 482 |
| Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val |     |
| 145 150 155   |     |
| CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG | 530 |
| Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys |     |

09564678 092804



| 160 |     |     |     |     |     |     |     |     |     | 165 |            |            |     |     | 170 |      |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|------------|-----|-----|-----|------|--|--|--|--|
| CAT | CCT | CCT | GCC | TCA | GCC | TCC | CAA | GTA | GCT | GGG | ACC        | AAA        | GAC | ATG | CAC | 578  |  |  |  |  |
| His | Pro | Pro | Ala | Ser | Ala | Ser | Gln | Val | Ala | Gly | Thr        | Lys        | Asp | Met | His |      |  |  |  |  |
|     |     | 175 |     |     |     |     | 180 |     |     |     |            | 185        |     |     |     |      |  |  |  |  |
| CAC | TAC | ACC | TGG | CTA | ATT | TTT | ATT | TTT | ATT | TTT | AAT        | TTT        | TTG | AGA | CAG | 626  |  |  |  |  |
| His | Tyr | Thr | Trp | Leu | Ile | Phe | Ile | Phe | Ile | Phe | Asn        | Phe        | Leu | Arg | Gln |      |  |  |  |  |
|     | 190 |     |     |     |     | 195 |     |     |     |     | 200        |            |     |     |     |      |  |  |  |  |
| AGT | CTC | AAC | TCT | GTC | ACC | CAG | GCT | GGA | GTG | CAG | TGG        | CGC        | AAT | CTT | GGC | 674  |  |  |  |  |
| Ser | Leu | Asn | Ser | Val | Thr | Gln | Ala | Gly | Val | Gln | Trp        | Arg        | Asn | Leu | Gly |      |  |  |  |  |
| 205 |     |     |     |     | 210 |     |     |     |     | 215 |            |            |     |     | 220 |      |  |  |  |  |
| TCA | CTG | CAA | CCT | CTG | CCT | CCC | GGG | TTC | AAG | TTA | TTC        | TCC        | TGC | CCC | AGC | 722  |  |  |  |  |
| Ser | Leu | Gln | Pro | Leu | Pro | Pro | Gly | Phe | Lys | Leu | Phe        | Ser        | Cys | Pro | Ser |      |  |  |  |  |
|     |     |     |     | 225 |     |     |     |     | 230 |     |            |            |     | 235 |     |      |  |  |  |  |
| CTC | CTG | AGT | AGC | TGG | GAC | TAC | AGG | CGC | CCA | CCA | CGC        | CTA        | GCT | AAT | TTT | 770  |  |  |  |  |
| Leu | Leu | Ser | Ser | Trp | Asp | Tyr | Arg | Arg | Pro | Pro | Arg        | Leu        | Ala | Asn | Phe |      |  |  |  |  |
|     |     |     | 240 |     |     |     |     | 245 |     |     |            |            | 250 |     |     |      |  |  |  |  |
| TTT | GTA | TTT | TTA | GTA | GAG | ATG | GGG | TTC | ACC | ATG | TTC        | GCC        | AGG | TTG | ATC | 818  |  |  |  |  |
| Phe | Val | Phe | Leu | Val | Glu | Met | Gly | Phe | Thr | Met | Phe        | Ala        | Arg | Leu | Ile |      |  |  |  |  |
|     |     | 255 |     |     |     |     | 260 |     |     |     |            | 265        |     |     |     |      |  |  |  |  |
| TTG | ATC | TCT | GGA | CCT | TGT | GAT | CTG | CCT | GCC | TCG | GCC        | TCC        | CAA | AGT | GCT | 866  |  |  |  |  |
| Leu | Ile | Ser | Gly | Pro | Cys | Asp | Leu | Pro | Ala | Ser | Ala        | Ser        | Gln | Ser | Ala |      |  |  |  |  |
|     | 270 |     |     |     |     | 275 |     |     |     |     | 280        |            |     |     |     |      |  |  |  |  |
| GGG | ATT | ACA | GGC | GTG | AGC | CAC | CAC | GCC | CGG | CTT | ATT        | TTT        | AAT | TTT | TGT | 914  |  |  |  |  |
| Gly | Ile | Thr | Gly | Val | Ser | His | His | Ala | Arg | Leu | Ile        | Phe        | Asn | Phe | Cys |      |  |  |  |  |
| 285 |     |     |     |     | 290 |     |     |     |     | 295 |            |            |     |     | 300 |      |  |  |  |  |
| TTG | TTT | GAA | ATG | GAA | TCT | CAC | TCT | GTT | ACC | CAG | GCT        | GGA        | GTG | CAA | TGG | 962  |  |  |  |  |
| Leu | Phe | Glu | Met | Glu | Ser | His | Ser | Val | Thr | Gln | Ala        | Gly        | Val | Gln | Trp |      |  |  |  |  |
|     |     |     |     | 305 |     |     |     |     | 310 |     |            |            |     | 315 |     |      |  |  |  |  |
| CCA | AAT | CTC | GGC | TCA | CTG | CAA | CCT | CTG | CCT | CCC | GGG        | CTC        | AAG | CGA | TTC | 1010 |  |  |  |  |
| Pro | Asn | Leu | Gly | Ser | Leu | Gln | Pro | Leu | Pro | Pro | Gly        | Leu        | Lys | Arg | Phe |      |  |  |  |  |
|     |     |     | 320 |     |     |     |     | 325 |     |     |            |            | 330 |     |     |      |  |  |  |  |
| TCC | TGT | CTC | AGC | CTC | CCA | AGC | AGC | TGG | GAT | TAC | GGG        | CAC        | CTG | CCA | CCA | 1058 |  |  |  |  |
| Ser | Cys | Leu | Ser | Leu | Pro | Ser | Ser | Trp | Asp | Tyr | Gly        | His        | Leu | Pro | Pro |      |  |  |  |  |
|     |     | 335 |     |     |     |     | 340 |     |     |     |            | 345        |     |     |     |      |  |  |  |  |
| CAC | CCC | GCT | AAT | TTT | TGT | ATT | TTC | ATT | AGA | GGC | GGG        | GTT        | TCA | CCA | TAT | 1106 |  |  |  |  |
| His | Pro | Ala | Asn | Phe | Cys | Ile | Phe | Ile | Arg | Gly | Gly        | Val        | Ser | Pro | Tyr |      |  |  |  |  |
|     | 350 |     |     |     |     | 355 |     |     |     |     | 360        |            |     |     |     |      |  |  |  |  |
| TTG | TCA | GGC | TGG | TCT | CAA | ACT | CCT | GAC | CTC | AGG | TGACCCACCT | GCCTCAGCCT |     |     |     | 1159 |  |  |  |  |
| Leu | Ser | Gly | Trp | Ser | Gln | Thr | Pro | Asp | Leu | Arg |            |            |     |     |     |      |  |  |  |  |



AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCAGGC TGGTCTCAAA CTTCTGGCTT 1279  
 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTSTA AACAGTTACA 1339  
 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA 1399  
 GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA 1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile  
 1 5 10 15  
 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala  
 20 25 30  
 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg  
 35 40 45  
 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly  
 50 55 60  
 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala  
 65 70 75 80  
 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu  
 85 90 95  
 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp  
 100 105 110  
 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp  
 115 120 125  
 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu  
 130 135 140  
 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp  
 145 150 155 160  
 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala  
 165 170 175  
 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp  
 180 185 190

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Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser  
195 200 205

Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro  
210 215 220

Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser  
225 230 235 240

Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu  
245 250 255

Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly  
260 265 270

Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly  
275 280 285

Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met  
290 295 300

Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly  
305 310 315 320

Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser  
325 330 335

Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn  
340 345 350

Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp  
355 360 365

Ser Gln Thr Pro Asp Leu Arg  
370 375

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT 60

CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120

AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTITAGTA 180



GAGATGGAGT TTAACCTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240  
TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCCTC 300  
TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCCTGA TGTTGCCCAA GCTGGTCTCC 360  
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGTCAGCC 420  
GTGCCTGGCC TTTTATTTT ATTTTATTTT AGACACAGGT GTACCACTCT TACCCAGGAT 480  
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540  
TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600  
TTTATTTTAA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660  
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC 720  
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTGTAT 780  
TTTGTAGTAG GATGGGGTTT CACCATGTTT GCCAGGTTGA TCTGATCTC TTGACCTTGT 840  
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900  
CTATTTTAA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960  
AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGG TCAAGCGATT CTCCTGTCTC 1020  
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080  
CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140  
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200  
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260  
TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320  
TTTAAACAG TTACATCTTT ATTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380  
C 1381

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1418 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:



|  |      |
|--|------|
| TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT | 60   |
| CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC  | 120  |
| AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT  | 180  |
| AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT  | 240  |
| CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT  | 300  |
| GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT  | 360  |
| CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC   | 420  |
| TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT  | 480  |
| GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC  | 540  |
| TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTAT  | 600  |
| TTTTATTTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG  | 660  |
| GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG  | 720  |
| CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT  | 780  |
| AGTAGAGATG GGGTTTCACC ATGTTCGCCA GGTGATGCT AGATCTCTTG ACCTTGATG    | 840  |
| CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC  | 900  |
| TATTTTTAAT TTTTGTGTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA  | 960  |
| ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT  | 1020 |
| CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCCGCTAA TTTTGTATT   | 1080 |
| TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAACTCC TGACCTCAGG   | 1140 |
| TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCGTGACGC CTCACCCAGC  | 1200 |
| CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG  | 1260 |
| GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC   | 1320 |
| ATTTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG  | 1380 |
| AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT                          | 1418 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

0996478-092801  
TOPSECRET



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

09964678-093801



(ii) MOLECULE TYPE: cDNA

14

(ii) MOLECULE TYPE: cDNA

14

(ii) MOLECULE TYPE: cDNA

14



# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne  
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
Screening Drugs Effective for the Treatment or Prevention  
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
  - (B) STREET: 1100 New York Ave., Suite 600
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Esmond, Robert W.
  - (B) REGISTRATION NUMBER: 32,893
  - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-371-2600
  - (B) TELEFAX: 202-371-2540

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1442 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 15..1139
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC  
 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys  
 1 5 10



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAT | GGC | GCA | ATC | TCA | GCT | CAC | CGC | AAC | CTC | CGC | CTC | CCG | GGT | TCA | AGC | 98  |
| Asn | Gly | Ala | Ile | Ser | Ala | His | Arg | Asn | Leu | Arg | Leu | Pro | Gly | Ser | Ser |     |
|     |     | 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |
| GAT | TCT | CCT | GCC | TCA | GCC | TCC | CCA | GTA | GCT | GGG | ATT | ACA | GGC | ATG | TGC | 146 |
| Asp | Ser | Pro | Ala | Ser | Ala | Ser | Pro | Val | Ala | Gly | Ile | Thr | Gly | Met | Cys |     |
|     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |
| ACC | CAC | GCT | CGG | CTA | ATT | TTG | TAT | TTT | TTT | TTA | GTA | GAG | ATG | GAG | TTT | 194 |
| Thr | His | Ala | Arg | Leu | Ile | Leu | Tyr | Phe | Phe | Leu | Val | Glu | Met | Glu | Phe |     |
|     | 45  |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |
| CTC | CAT | GTT | GGT | CAG | GCT | GGT | CTC | GAA | CTC | CCG | ACC | TCA | GAT | GAT | CCC | 242 |
| Leu | His | Val | Gly | Gln | Ala | Gly | Leu | Glu | Leu | Pro | Thr | Ser | Asp | Asp | Pro |     |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |
| TCC | GTC | TCG | GCC | TCC | CAA | AGT | GCT | AGA | TAC | AGG | ACT | GGC | CAC | CAT | GCC | 290 |
| Ser | Val | Ser | Ala | Ser | Gln | Ser | Ala | Arg | Tyr | Arg | Thr | Gly | His | His | Ala |     |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     |     | 90  |     |     |
| CGG | CTC | TGC | CTG | GCT | AAT | TTT | TGT | GGT | AGA | AAC | AGG | GTT | TCA | CTG | ATG | 338 |
| Arg | Leu | Cys | Leu | Ala | Asn | Phe | Cys | Gly | Arg | Asn | Arg | Val | Ser | Leu | Met |     |
|     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |
| TGC | CCA | AGC | TGG | TCT | CCT | GAG | CTC | AAG | CAG | TCC | ACC | TGC | CTC | AGC | CTC | 386 |
| Cys | Pro | Ser | Trp | Ser | Pro | Glu | Leu | Lys | Gln | Ser | Thr | Cys | Leu | Ser | Leu |     |
|     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |
| CCA | AAG | TGC | TGG | GAT | TAC | AGG | CGT | GCA | GCC | GTG | CCT | GGC | CTT | TTT | ATT | 434 |
| Pro | Lys | Cys | Trp | Asp | Tyr | Arg | Arg | Ala | Ala | Val | Pro | Gly | Leu | Phe | Ile |     |
|     | 125 |     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |
| TTA | TTT | TTT | TTA | AGA | CAC | AGG | TGT | CCC | ACT | CTT | ACC | CAG | GAT | GAA | GTG | 482 |
| Leu | Phe | Phe | Leu | Arg | His | Arg | Cys | Pro | Thr | Leu | Thr | Gln | Asp | Glu | Val |     |
|     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |
| CAG | TGG | TGT | GAT | CAC | AGC | TCA | CTG | CAG | CCT | TCA | ACT | CCT | GAG | ATC | AAG | 530 |
| Gln | Trp | Cys | Asp | His | Ser | Ser | Leu | Gln | Pro | Ser | Thr | Pro | Glu | Ile | Lys |     |
|     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |
| CAT | CCT | CCT | GCC | TCA | GCC | TCC | CAA | GTA | GCT | GGG | ACC | AAA | GAC | ATG | CAC | 578 |
| His | Pro | Pro | Ala | Ser | Ala | Ser | Gln | Val | Ala | Gly | Thr | Lys | Asp | Met | His |     |
|     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |
| CAC | TAC | ACC | TGG | CTA | ATT | TTT | ATT | TTT | ATT | TTT | AAT | TTT | TTG | AGA | CAG | 626 |
| His | Tyr | Thr | Trp | Leu | Ile | Phe | Ile | Phe | Ile | Phe | Asn | Phe | Leu | Arg | Gln |     |
|     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     |     |     |
| AGT | CTC | AAC | TCT | GTC | ACC | CAG | GCT | GGA | GTG | CAG | TGG | CGC | AAT | CTT | GGC | 674 |
| Ser | Leu | Asn | Ser | Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Arg | Asn | Leu | Gly |     |
|     | 205 |     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |
| TCA | CTG | CAA | CCT | CTG | CCT | CCC | GGG | TTC | AAG | TTA | TTC | TCC | TGC | CCC | AGC | 722 |
| Ser | Leu | Gln | Pro | Leu | Pro | Pro | Gly | Phe | Lys | Leu | Phe | Ser | Cys | Pro | Ser |     |
|     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |
| CTC | CTG | AGT | AGC | TGG | GAC | TAC | AGG | CGC | CCA | CCA | CGC | CTA | GCT | AAT | TTT | 770 |
| Leu | Leu | Ser | Ser | Trp | Asp | Tyr | Arg | Arg | Pro | Pro | Arg | Leu | Ala | Asn | Phe |     |
|     |     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |
| TTT | GTA | TTT | TTA | GTA | GAG | ATG | GGG | TTC | ACC | ATG | TTC | GCC | AGG | TTG | ATC | 818 |
| Phe | Val | Phe | Leu | Val | Glu | Met | Gly | Phe | Thr | Met | Phe | Ala | Arg | Leu | Ile |     |
|     |     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |
| TTG | ATC | TCT | GGA | CCT | TGT | GAT | CTG | CCT | GCC | TCG | GCC | TCC | CAA | AGT | GCT | 866 |



|            |            |            |            |             |            |     |     |     |     |     |            |            |     |     |     |  |      |
|------------|------------|------------|------------|-------------|------------|-----|-----|-----|-----|-----|------------|------------|-----|-----|-----|--|------|
| Leu        | Ile        | Ser        | Gly        | Pro         | Cys        | Asp | Leu | Pro | Ala | Ser | Ala        | Ser        | Gln | Ser | Ala |  |      |
| 270        |            |            |            |             |            | 275 |     |     |     |     | 280        |            |     |     |     |  |      |
| GGG        | ATT        | ACA        | GGC        | GTG         | AGC        | CAC | CAC | GCC | CGG | CTT | ATT        | TTT        | AAT | TTT | TGT |  | 914  |
| Gly        | Ile        | Thr        | Gly        | Val         | Ser        | His | His | Ala | Arg | Leu | Ile        | Phe        | Asn | Phe | Cys |  |      |
| 285        |            |            |            |             | 290        |     |     |     |     | 295 |            |            |     |     | 300 |  |      |
| TTG        | TTT        | GAA        | ATG        | GAA         | TCT        | CAC | TCT | GTT | ACC | CAG | GCT        | GGA        | GTG | CAA | TGG |  | 962  |
| Leu        | Phe        | Glu        | Met        | Glu         | Ser        | His | Ser | Val | Thr | Gln | Ala        | Gly        | Val | Gln | Trp |  |      |
|            |            |            |            | 305         |            |     |     |     | 310 |     |            |            |     | 315 |     |  |      |
| CCA        | AAT        | CTC        | GGC        | TCA         | CTG        | CAA | CCT | CTG | CCT | CCC | GGG        | CTC        | AAG | CGA | TTC |  | 1010 |
| Pro        | Asn        | Leu        | Gly        | Ser         | Leu        | Gln | Pro | Leu | Pro | Pro | Gly        | Leu        | Lys | Arg | Phe |  |      |
|            |            |            | 320        |             |            |     |     | 325 |     |     |            |            | 330 |     |     |  |      |
| TCC        | TGT        | CTC        | AGC        | CTC         | CCA        | AGC | AGC | TGG | GAT | TAC | GGG        | CAC        | CTG | CCA | CCA |  | 1058 |
| Ser        | Cys        | Leu        | Ser        | Leu         | Pro        | Ser | Ser | Trp | Asp | Tyr | Gly        | His        | Leu | Pro | Pro |  |      |
|            |            | 335        |            |             |            |     | 340 |     |     |     |            | 345        |     |     |     |  |      |
| CAC        | CCC        | GCT        | AAT        | TTT         | TGT        | ATT | TTC | ATT | AGA | GGC | GGG        | GTT        | TCA | CCA | TAT |  | 1106 |
| His        | Pro        | Ala        | Asn        | Phe         | Cys        | Ile | Phe | Ile | Arg | Gly | Gly        | Val        | Ser | Pro | Tyr |  |      |
|            | 350        |            |            |             |            | 355 |     |     |     |     | 360        |            |     |     |     |  |      |
| TTG        | TCA        | GGC        | TGG        | TCT         | CAA        | ACT | CCT | GAC | CTC | AGG | TGACCCACCT | GCCTCAGCCT |     |     |     |  | 1159 |
| Leu        | Ser        | Gly        | Trp        | Ser         | Gln        | Thr | Pro | Asp | Leu | Arg |            |            |     |     |     |  |      |
| 365        |            |            |            |             | 370        |     |     |     |     | 375 |            |            |     |     |     |  |      |
| TCCAAAGTGC | TGGGATTACA | GGCGTGAGCC | ACCTCACCCA | GCCGGCTAAT  | TTAGATAAAA |     |     |     |     |     |            |            |     |     |     |  | 1219 |
| AAATATGTAG | CAATGGGGGG | TCTTGCTATG | TTGCCCAGGC | TGGTCTCAAA  | CTTCTGGCTT |     |     |     |     |     |            |            |     |     |     |  | 1279 |
| CATGCAATCC | TTCCAAATGA | GCCACAACAC | CCAGCCAGTC | ACATTTTTTTA | AACAGTTACA |     |     |     |     |     |            |            |     |     |     |  | 1339 |
| TCTTTATTTT | AGTATACTAG | AAAGTAATAC | AATAAACATG | TCAAACCTGC  | AAATTCAGTA |     |     |     |     |     |            |            |     |     |     |  | 1399 |
| GTAACAGAGT | TCTTTTATAA | CTTTTAAACA | AAGCTTTAGA | GCA         |            |     |     |     |     |     |            |            |     |     |     |  | 1442 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Glu | Phe | Ser | Leu | Leu | Leu | Pro | Arg | Leu | Glu | Cys | Asn | Gly | Ala | Ile |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Ala | His | Arg | Asn | Leu | Arg | Leu | Pro | Gly | Ser | Ser | Asp | Ser | Pro | Ala |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ser | Ala | Ser | Pro | Val | Ala | Gly | Ile | Thr | Gly | Met | Cys | Thr | His | Ala | Arg |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Leu | Ile | Leu | Tyr | Phe | Phe | Leu | Val | Glu | Met | Glu | Phe | Leu | His | Val | Gly |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Gln | Ala | Gly | Leu | Glu | Leu | Pro | Thr | Ser | Asp | Asp | Pro | Ser | Val | Ser | Ala |  |  |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |
| Ser | Gln | Ser | Ala | Arg | Tyr | Arg | Thr | Gly | His | His | Ala | Arg | Leu | Cys | Leu |  |  |



| 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Phe | Cys | Gly | Arg | Asn | Arg | Val | Ser | Leu | Met | Cys | Pro | Ser | Trp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Pro | Glu | Leu | Lys | Gln | Ser | Thr | Cys | Leu | Ser | Leu | Pro | Lys | Cys | Trp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Tyr | Arg | Arg | Ala | Ala | Val | Pro | Gly | Leu | Phe | Ile | Leu | Phe | Phe | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Arg | His | Arg | Cys | Pro | Thr | Leu | Thr | Gln | Asp | Glu | Val | Gln | Trp | Cys | Asp |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| His | Ser | Ser | Leu | Gln | Pro | Ser | Thr | Pro | Glu | Ile | Lys | His | Pro | Pro | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | Ala | Ser | Gln | Val | Ala | Gly | Thr | Lys | Asp | Met | His | His | Tyr | Thr | Trp |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Ile | Phe | Ile | Phe | Ile | Phe | Asn | Phe | Leu | Arg | Gln | Ser | Leu | Asn | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Arg | Asn | Leu | Gly | Ser | Leu | Gln | Pro |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Pro | Pro | Gly | Phe | Lys | Leu | Phe | Ser | Cys | Pro | Ser | Leu | Leu | Ser | Ser |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Trp | Asp | Tyr | Arg | Arg | Pro | Pro | Arg | Leu | Ala | Asn | Phe | Phe | Val | Phe | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Glu | Met | Gly | Phe | Thr | Met | Phe | Ala | Arg | Leu | Ile | Leu | Ile | Ser | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Pro | Cys | Asp | Leu | Pro | Ala | Ser | Ala | Ser | Gln | Ser | Ala | Gly | Ile | Thr | Gly |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Val | Ser | His | His | Ala | Arg | Leu | Ile | Phe | Asn | Phe | Cys | Leu | Phe | Glu | Met |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Glu | Ser | His | Ser | Val | Thr | Gln | Ala | Gly | Val | Gln | Trp | Pro | Asn | Leu | Gly |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Ser | Leu | Gln | Pro | Leu | Pro | Pro | Gly | Leu | Lys | Arg | Phe | Ser | Cys | Leu | Ser |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Leu | Pro | Ser | Ser | Trp | Asp | Tyr | Gly | His | Leu | Pro | Pro | His | Pro | Ala | Asn |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Phe | Cys | Ile | Phe | Ile | Arg | Gly | Gly | Val | Ser | Pro | Tyr | Leu | Ser | Gly | Trp |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Gln | Thr | Pro | Asp | Leu | Arg |     |     |     |     |     |     |     |     |     |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|  |      |
|--|------|
| TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT | 60   |
| CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC  | 120  |
| AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA  | 180  |
| GAGATGGAGT TTAACCTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC | 240  |
| TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC  | 300  |
| TGCCTGGCTA ATTTTTGTGG TAGAAACAGG GTTTCACTGA TGTTGCCCAA GCTGGTCTCC  | 360  |
| TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGTCAGCC   | 420  |
| GTGCCTGGCC TTTTATATTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT  | 480  |
| GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC  | 540  |
| TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT  | 600  |
| TTTATTTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC | 660  |
| AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC  | 720  |
| CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTTGTAT  | 780  |
| TTTTAGTAGA GATGGGGTTT CACCATGTTT GCCAGGTTGA TCTTGATCTC TTGACCTTGT  | 840  |
| GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC  | 900  |
| CTATTTTTTAA TTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC  | 960  |
| AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC  | 1020 |
| AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT  | 1080 |
| CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA  | 1140 |
| CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC  | 1200 |
| GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC  | 1260 |
| TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT  | 1320 |
| TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA  | 1380 |
| C  | 1381 |

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|             |            |            |            |            |             |      |
|-------------|------------|------------|------------|------------|-------------|------|
| TTTTTTTTTTT | GAGATGGAGT | TTTCGCTCTT | GTTGCCCAGG | CTGGAGTGCA | ATGGCGCAAT  | 60   |
| CTCAGCTCAC  | CGCAACCTCC | GCCTCCCGGG | TTCAAGCGAT | TCTCCTGCCT | CAGCCTCCCC  | 120  |
| AGTAGGCTGG  | GATTACAGGC | ATGTGCACCA | CGCTCGGCTA | ATTTTGTATT | TTTTTTTAGT  | 180  |
| AGAGATGGAG  | TTTCTCCATG | TTGGTCAGGC | TGGTCTCGAA | CTCCGACCTC | AGATGATCCT  | 240  |
| CCCGTCTCGG  | CCTCCCAAAG | TGCTAGATAC | AGGACTGAGC | ACCATGCCCC | GCCTCTGCCT  | 300  |
| GGCTAATTTT  | TGTGGTAGAA | ACAGGGTTTC | ACTGATGTGC | CCAAGCTGGT | CTCCTGAGCT  | 360  |
| CAAGCAGTCC  | ACCTGCCTCA | GCCTCCCAA  | GTGCTGGGAT | TACAGGCGTG | CAGCCGTGCC  | 420  |
| TGGCCTTTTT  | ATTTTATTTT | TTTTAAGACA | CAGGTGTCCC | ACTCTTACCC | AGGATGAAGT  | 480  |
| GCAGTGGTGT  | GATCACAGCT | CACTGCAGCC | TTCAACTCTG | AGATCAAGCA | TCCTCCTGCC  | 540  |
| TCAGCCTCCC  | AAAGTAGCTG | GGACCAAAGA | CATGCACCAC | TACACCTGGC | TAATTTTTAT  | 600  |
| TTTTATTTTT  | AATTTTTTGA | GACAGAGTCT | CAACTCTGTC | ACCCAGGCTG | GAGTGCAGTG  | 660  |
| GCGCAATCTT  | GGCTCACTGC | AACCTCTGCC | TCCCGGGTTC | AAGTTATTCT | CCTGCCCCAG  | 720  |
| CCTCCTGAGT  | AGCTGGGACT | ACAGGCGCCC | ACCACGCCTA | GCTAATTTTT | TTGTATTTTT  | 780  |
| AGTAGAGATG  | GGGTTTCACC | ATGTTCGCCA | GGTTGATGCT | AGATCTCTTG | ACCTTGTGAT  | 840  |
| CTGCCTGCCT  | CGGCCTCCCA | AAGTGCTGGG | ATTACAGGAC | GTGACGCCCA | CCGCCC GGCC | 900  |
| TATTTTTAAT  | TTTTGTTTGT | TTGAAATGGA | ATCTCACTCT | GTTACCCAGG | CTGGAGTGCA  | 960  |
| ATGGCCAAAT  | CTCGGCTCAC | TGCAACCTCT | GCCTCCCGGG | CTCAAGCGAT | TCTCCTGTCT  | 1020 |
| CAGCCTCCCA  | AGCAGCTGGG | ATTACGGGCA | CCTGCACCAC | ACCCCGCTAA | TTTTTGTATT  | 1080 |
| TTCATTAGAG  | GCGGGGTTTC | ACCATATTTG | TCAGGCTGGT | CTCAAACCTC | TGACCTCAGG  | 1140 |
| TGACCCACCT  | GCCTCAGCCT | TCCAAAGTGC | TGGGATTACA | GGCGTGACGC | CTCACCAGC   | 1200 |
| CGGCTAATTT  | AGATAAAAAA | ATATGTAGCA | ATGGGGGGTC | TTGCTATGTT | GCCCAGGCTG  | 1260 |
| GTCTCAAAC   | TCTGGCTTCA | TGCAATCCTT | CCAAATGAGC | CACAACACCC | AGCCAGTCAC  | 1320 |
| ATTTTAAAC   | AGTTACATCT | TTATTTTAGT | ATACTAGAAA | GTGATACGAT | AACATGGCGG  | 1380 |
| AACCTGCAAA  | TTGAGTAGT  | ACAGAGTCTT | TTATAACT   |            |             | 1418 |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:



TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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T08260-B2949563



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

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